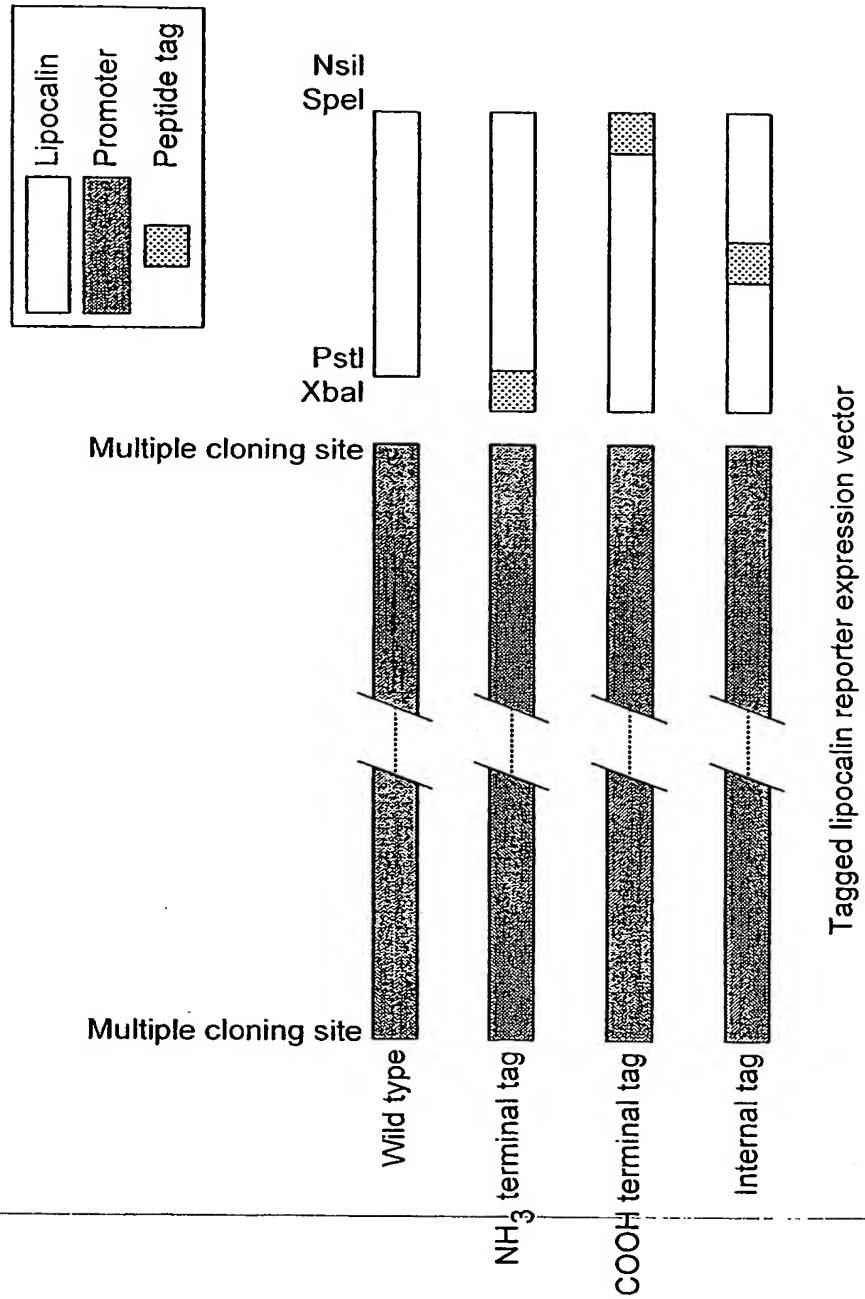

FIG. 1

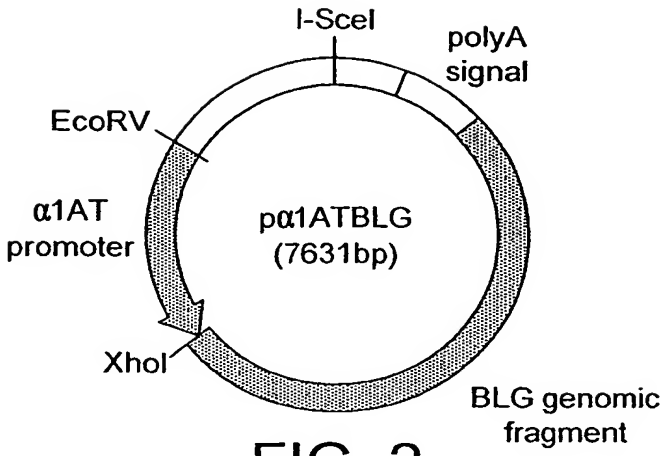
I-SceI
polyA signal
EcoRV
α1AT promoter
pα1ATBLG (7631bp)
XhoI
BLG genomic fragment

FIG. 2

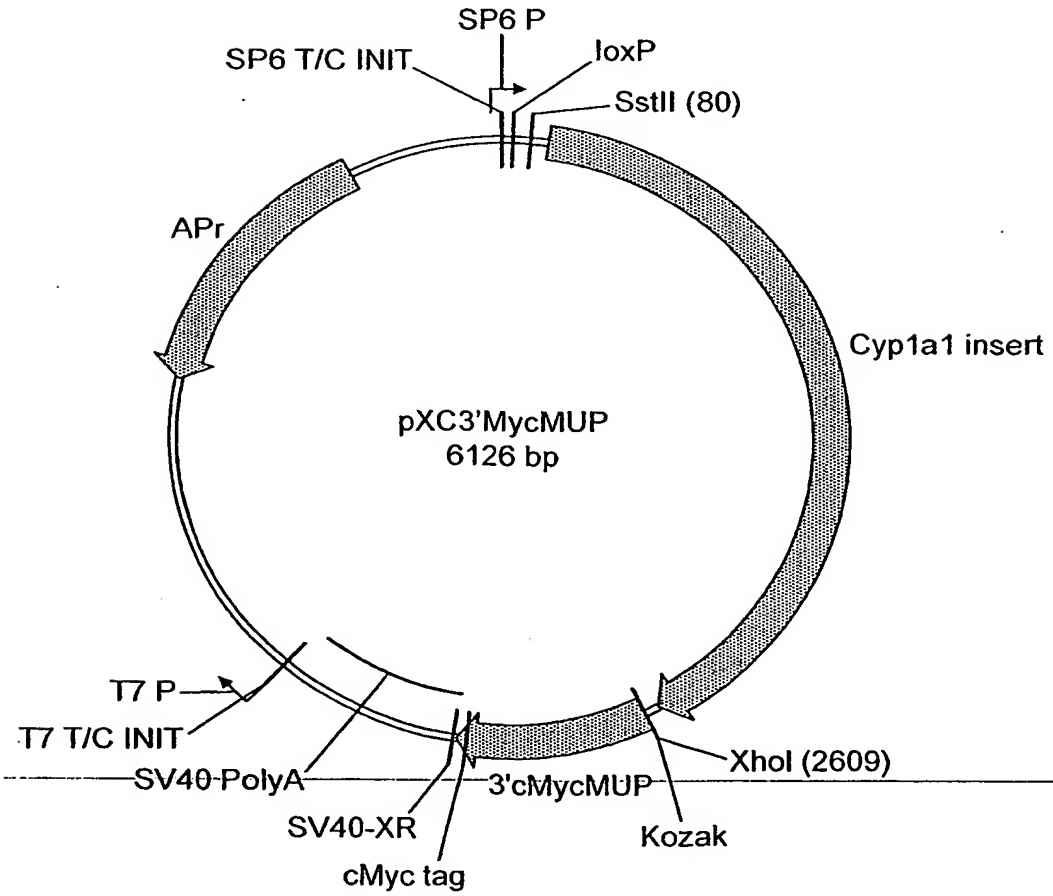
SP6 P
SP6 T/C INIT
loxP
SstII (80)
APr
Cyp1a1 insert
pXC3'MycMUP 6126 bp
T7 P
T7 T/C INIT
SV40-PolyA
3'cMycMUP
XhoI (2609)
SV40-XR
Kozak
cMyc tag

FIG. 3

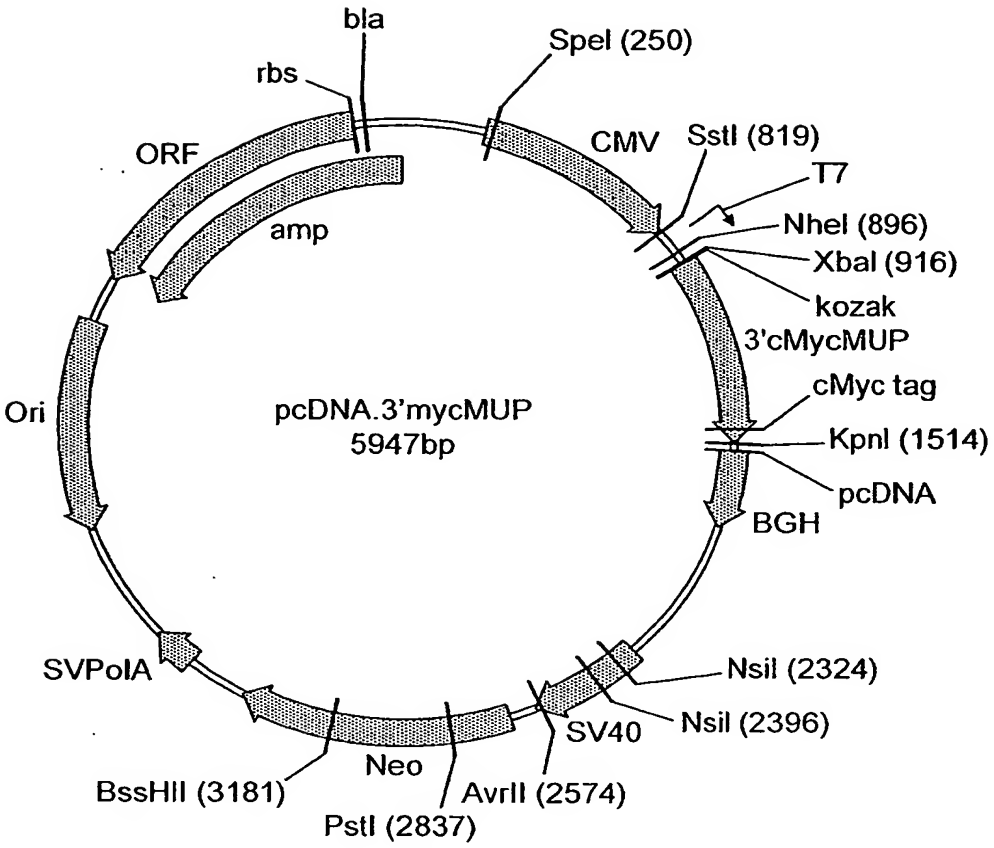
bla
rbs
ORF
amp
SpeI (250)
CMV
SstI (819)
T7
NheI (896)
XbaI (916)
kozak
3'cMycMUP
cMyc tag
KpnI (1514)
pcDNA
BGH
pcDNA.3'mycMUP
5947bp
Ori
SVPolA
NsiI (2324)
NsiI (2396)
SV40
Neo
BssHII (3181)
AvrII (2574)
PstI (2837)

FIG. 4

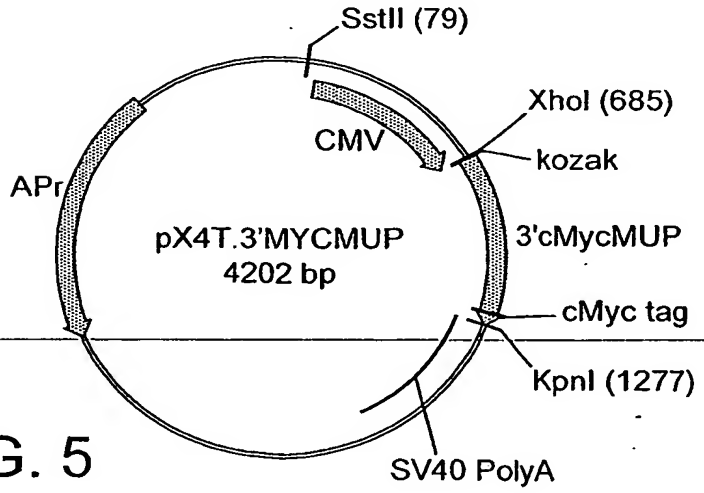
SstII (79)
XhoI (685)
CMV
kozak
APr
pX4T.3'MYCMUP
4202 bp
3'cMycMUP
cMyc tag
KpnI (1277)
SV40 PolyA

FIG. 5

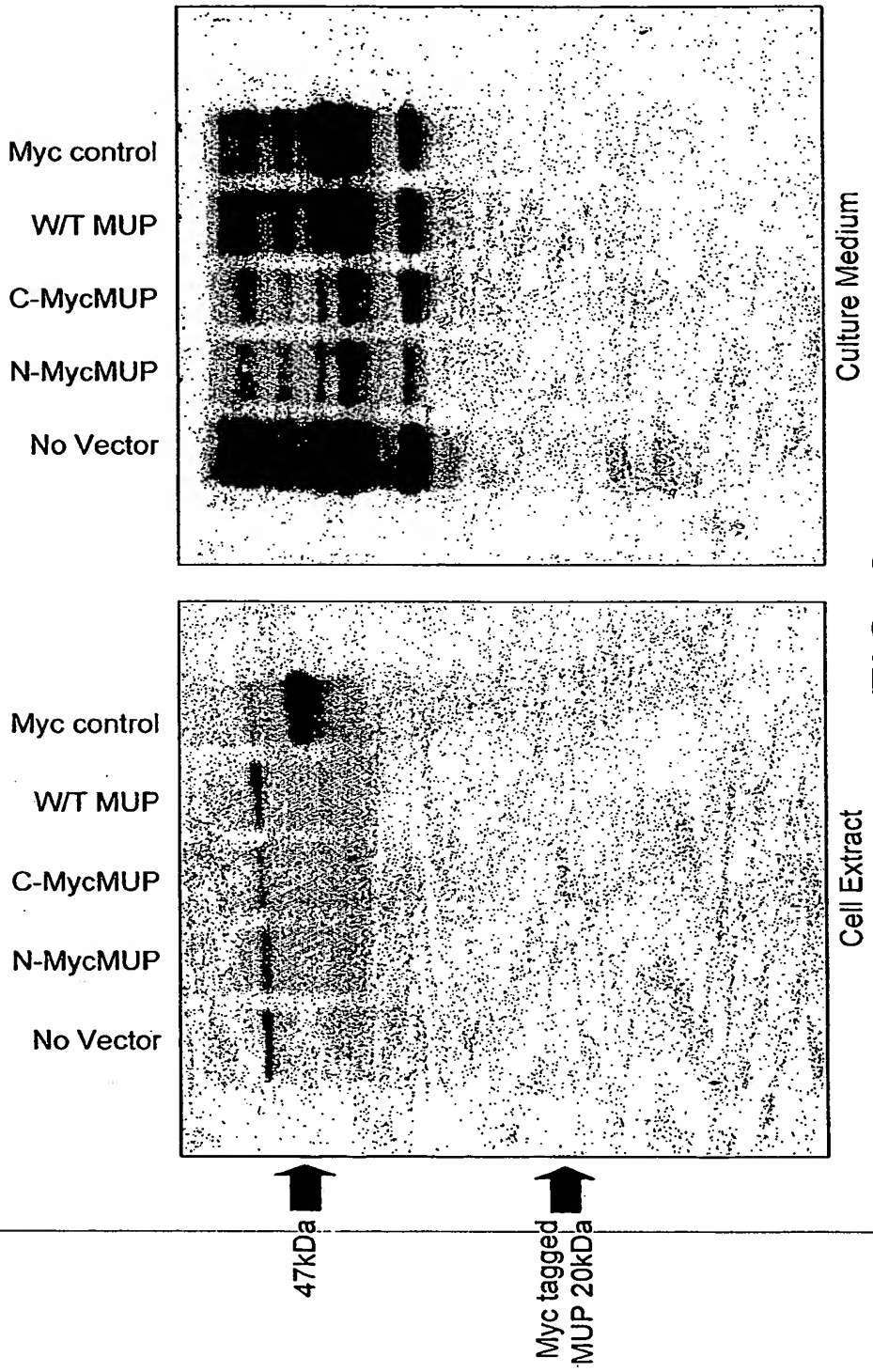
Myc control
W/T MUP
C-MycMUP
N-MycMUP
No Vector
Culture Medium
Myc control
W/T MUP
C-MycMUP
N-MycMUP
No Vector
Cell Extract
47kDa
Myc tagged MUP 20kDa

FIG. 6

```
      MetLysMetLeuLeuLeuLeuCysLeuGlyLeuThrLeuValCysValHisAlaGluGlu
  1   ATGAAGATGCTGCTGCTGCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAA
      AlaSerSerThrGlyArgAsnPheAsnValGluLysIleAsnGlyGluTrpHisThrIle
 61   GCTAGTTCTACGGGAAGGAACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATT
      IleLeuAlaSerAspLysArgGluLysIleGluAspAsnGlyAsnPheArgLeuPheLeu
121   ATCCTGGCCTCTGACAAAAGAGAAAAGATAGAAGATAATGGCAACTTTAGACTTTTTCTG
      GluGlnIleHisValLeuGluLysSerLeuValLeuLysPheHisThrValArgAspGlu
181   GAGCAAATCCATGTCTTGGAGAAATCCTTAGTTCTTAAATTCCATACTGTAAGAGATGAA
      GluCysSerGluLeuSerMetValAlaAspLysThrGluLysAlaGlyGluTyrSerVal
241   GAGTGCTCGGAATTATCTATGGTTGCTGACAAAACAGAAAAGGCTGGTGAATATTCTGTG
      ThrTyrAspGlyPheAsnThrPheThrIleProLysThrAspTyrAspAsnPheLeuMet
301   ACGTATGATGGATTCAATACATTTACTATACCTAAGACAGACTATGATAACTTTCTTATG
      AlaHisLeuIleAsnGluLysAspGlyGluThrPheGlnLeuMetGlyLeuTyrGlyArg
361   GCTCATCTCATTAACGAAAAGGATGGGGAAACCTTCCAGCTGATGGGGCTCTATGGCCGA
      GluProAspLeuSerSerAspIleLysGluArgPheAlaGlnLeuCysGluLysHisGly
421   GAACCAGATTTGAGTTCAGACATCAAGGAAAGGTTTGCACAACTATGTGAGAAGCATGGA
      IleLeuArgGluAsnIleIleAspLeuSerAsnAlaAsnArgCysLeuGlnAlaArgGlu
481   ATCCTTAGAGAAAATATCATTGACCTATCCAATGCCAATCGCTGCCTCCAGGCCCGAGAA
      ***
541   TGA
```

FIG. 7

```
      GlyProLeuGlySerMetGluGlnLysLeuIleSerGluGluAspLeuThrMetGluAla
  1   GGGCCCCTGGGATCCATGGAGCAGAAACTCATCTCTGAAGAGGATCTGACCATGGAAGCT
      SerSerThrGlyArgAsnPheAsnValGluLysIleAsnGlyGluTrpHisThrIleIle
 61   AGTTCTACGGGAAGGAACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATC
      LeuAlaSerAspLysArgGluLysIleGluAspAsnGlyAsnPheArgLeuPheLeuGlu
121   CTGGCCTCTGACAAAAGAGAAAAGATAGAAGATAATGGCAACTTTAGACTTTTTCTGGAG
      GlnIleHisValLeuGluLysSerLeuValLeuLysPheHisThrValArgAspGluGlu
181   CAAATCCATGTCTTGGAGAAATCCTTAGTTCTTAAATTCCATACTGTAAGAGATGAAGAG
      CysSerGluLeuSerMetValAlaAspLysThrGluLysAlaGlyGluTyrSerValThr
241   TGCTCGGAATTATCTATGGTTGCTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACG
      TyrAspGlyPheAsnThrPheThrIleProLysThrAspTyrAspAsnPheLeuMetAla
301   TATGATGGATTCAATACATTTACTATACCTAAGACAGACTATGATAACTTTCTTATGGCT
      HisLeuIleAsnGluLysAspGlyGluThrPheGlnLeuMetGlyLeuTyrGlyArgGlu
361   CATCTCATTAACGAAAAGGATGGGGAAACCTTCCAGCTGATGGGGCTCTATGGCCGAGAA
      ProAspLeuSerSerAspIleLysGluArgPheAlaGlnLeuCysGluLysHisGlyIle
421   CCAGATTTGAGTTCAGACATCAAGGAAAGGTTTGCACAACTATGTGAGAAGCATGGAATC
      LeuArgGluAsnIleIleAspLeuSerAsnAlaAsnArgCysLeuGlnAlaArgGlu***
481   CTTAGAGAAAATATCATTGACCTATCCAATGCCAATCGCTGCCTCCAGGCCCGAGAATGA
```

FIG. 8

*GlyProLeuGlySerMet*AlaIleIleValThrGlnThrMetLysGlyLeuAspIleGln
1 *GGGCCCCTGGGATCCATG*GCCATCATCGTCACCCAGACCATGAAAGGCCTGGACATCCAG
LysValAlaGlyThrTrpHisSerLeuAlaMetAlaAlaSerAspIleSerLeuLeuAsp
61 AAGGTGGCGGGGACTTGGCACTCCTTGGCTATGGCGGCCAGCGACATCTCCCTGCTGGAT
AlaGlnSerAlaProLeuArgValTyrValGluGluLeuLysProThrProGluGlyAsn
121 GCCCAGAGTGCCCCCCTGAGAGTGTACGTGGAGGAGCTGAAGCCCACCCCCGAGGGCAAC
LeuGluIleLeuLeuGlnLysTrpGluAsnGlyGluCysAlaGlnLysLysIleIleAla
181 CTGGAGATCCTGCTGCAGAAATGGGAGAACGGCGAGTGTGCTCAGAAGAAGATTATTGCA
GluLysThrLysIleProAlaValPheLysIleAspAlaLeuAsnGluAsnLysValLeu
241 GAAAAAACCAAGATCCCTGCGGTGTTCAAGATCGATGCCTTGAATGAGAACAAAGTCCTT
ValLeuAspThrAspTyrLysLysTyrLeuLeuPheCysMetGluAsnSerAlaGluPro
301 GTGCTGGACACCGACTACAAAAAGTACCTGCTCTTCTGCATGGAAAACAGTGCTGAGCCC
GluGlnSerLeuAlaCysGlnCysLeuValArgThrProGluValAspAsnGluAlaLeu
361 GAGCAAAGCCTGGCCTGCCAGTGCCTGGTCAGGACCCCGGAGGTGGACAACGAGGCCCTG
GluLysPheAspLysAlaLeuLysAlaLeuProMetHisIleArgLeuAlaPheAsnPro
421 GAGAAATTCGACAAAGCCCTCAAGGCCCTGCCCATGCACATCCGGCTTGCCTTCAACCCG
ThrGlnLeuGluGlyGlnCysHisVal**GluGlnLysLeuIleSerGluGluAspLeu*****
481 ACCCAGCTGGAGGGGCAGTGCCACGTC**GAGCAGAAACTCATCTCTGAAGAGGATCTG**TAG

FIG. 9

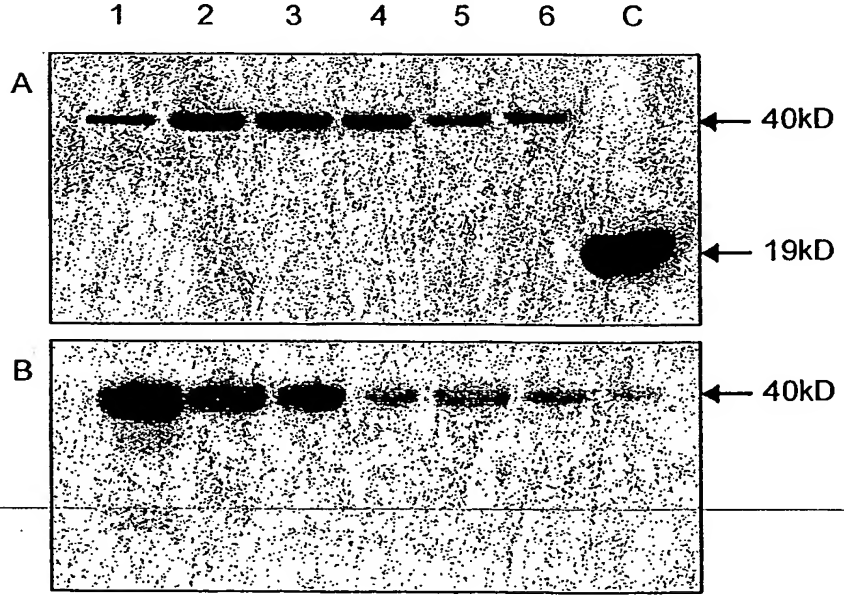

FIG. 10

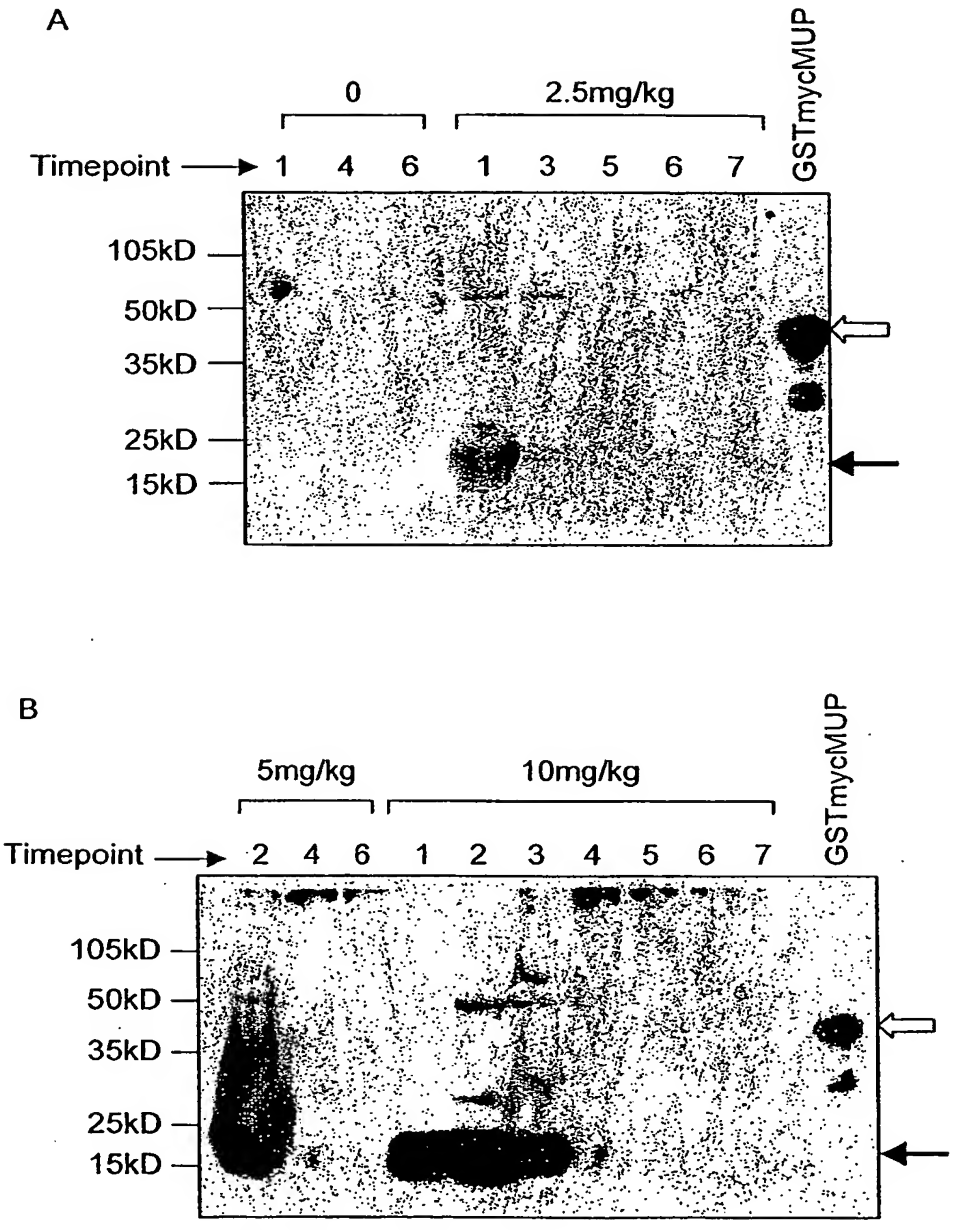
A
0
2.5mg/kg
GSTmycMUP
Timepoint
1 4 6 1 3 5 6 7
105kD
50kD
35kD
25kD
15kD
B
5mg/kg
10mg/kg
GSTmycMUP
Timepoint
2 4 6 1 2 3 4 5 6 7
105kD
50kD
35kD
25kD
15kD

FIG. 11

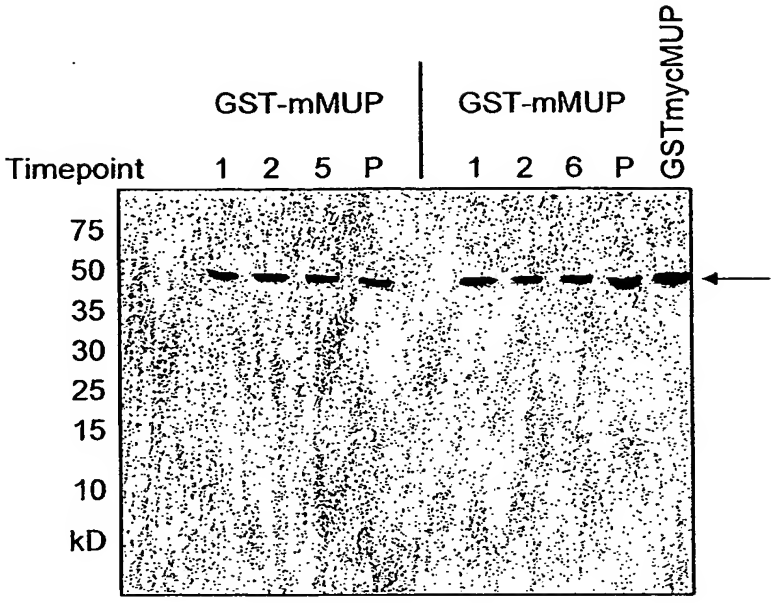
GST-mMUP
GST-mMUP
GSTmycMUP
Timepoint
1 2 5 P
1 2 6 P
75
50
35
30
25
15
10
kD

FIG. 12

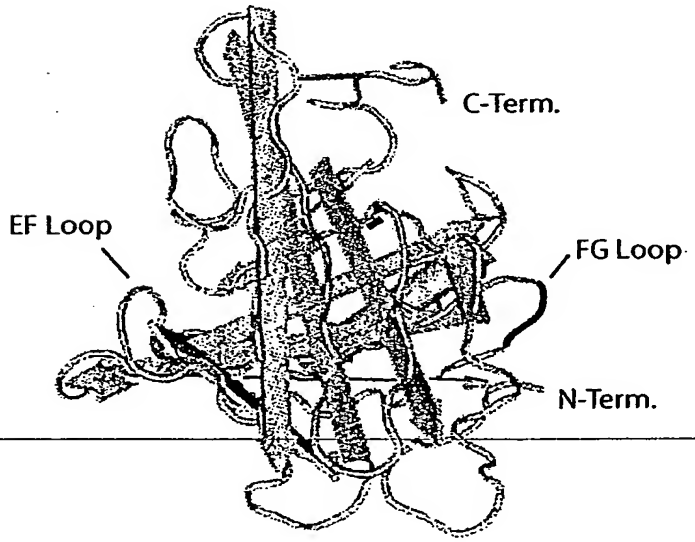
C-Term.
EF Loop
FG Loop
N-Term.

FIG. 13

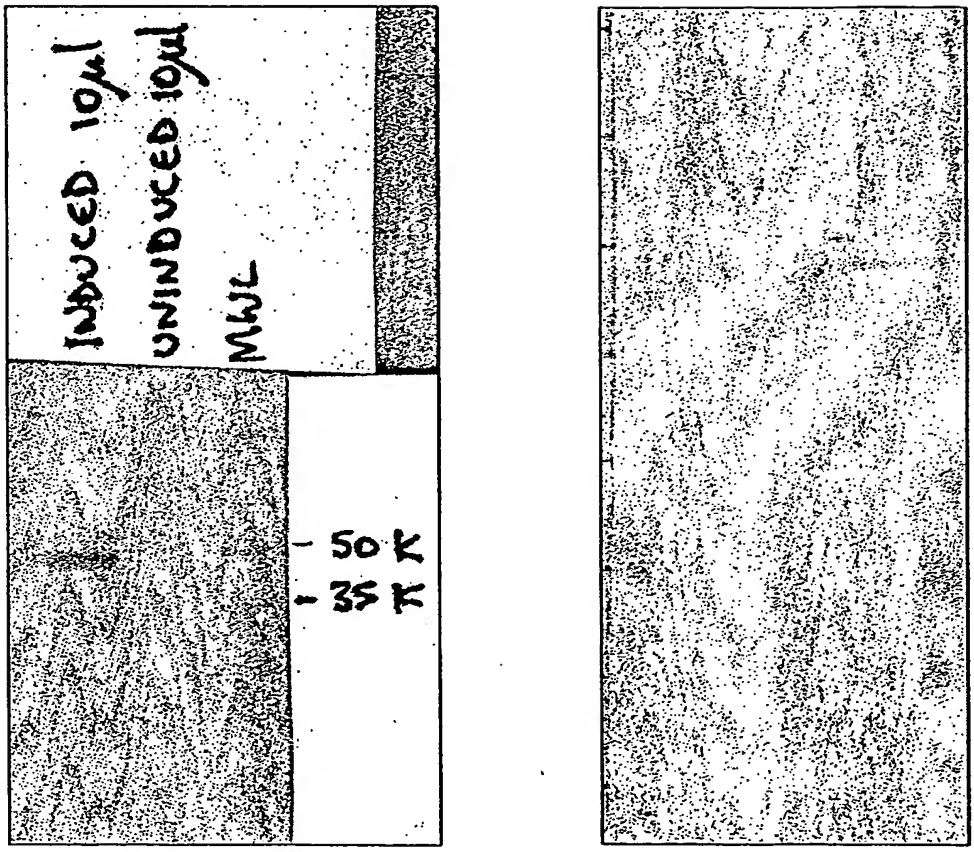

FIG. 14

```
                        +++++++++++++++++++++++++
1                                                                                                                100
SmMUP     (1)   METDTLLLWVLLLWVPGSTGDAAQPARRARRTKLGTELGSMEQKLISEEDLTMEASSTGRNFNVEKINGEWHTIILASDKREKIEDNGNFRLFLEQIHVL
SM        (1)   METDTLLLWVLLLWVPGSTGDAAQPAKMLLLLCLGLTLVCVH---------AEEASSTGRNFNVEKINGEWHTIILASDKREKIEDNGNFRLFLEQIHVL
SML       (1)   METDTLLLWVLLLWVPGSTGDAAQPAKMLLLLCLGLTLVCVH---------AEEASSTGRNFNVEKINGEWHTIILASDKREKIEDNGNFRLFLEQIHVL
SML100    (1)   METDTLLLWVLLLWVPGSTGDAAQPAKMLLLLCLGLTLVCVH---------AEEASSTGRNFNVEKINGEWHTIILASDKREKIEDNGNFRLFLEQIHVL

101                                                                                                              200
SmMUP     (101) EKSLVLKFHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYD----------------NFLMAHLINEKDGETFQLMGLYGREPDLSSDIKE
SM        (92)  EKSLVLKFHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYD----------------NFLMAHLINEKDGETFQLMGLYGREPDLSSDIKE
SML       (92)  EKSLVLKFHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDKL---GTGSSS---EFNFLMAHLINEKDGETFQLMGLYGREPDLSSDIKE
SML100    (92)  EKSLVLKFHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDKLNVRFSTIVRRRAEFNFLMAHLINEKDGETFQLMGLYGREPDLSSDIKE

201                                                         269
SmMUP     (185) RFAQLCEKHGILRENIIDLSNANRCLQARE------------------------------------------
SM        (176) RFAQLCEKHGILRENIIDLSNANRCLQAREEQKLISEEDLAAARGGPEQKLISEEDLNSAVDHHHHHH-
SML       (186) RFAQLCEKHGILRENIIDLSNANRCLQAREEQKLISEEDLAAARGGPEQKLISEEDLNSAVDHHHHHH-
SML100    (192) RFAQLCEKHGILRENIIDLSNANRCLQAREEQKLISEEDLAAARGGPEQKLISEEDLNSAVDHHHHHH-
```

FIG. 15

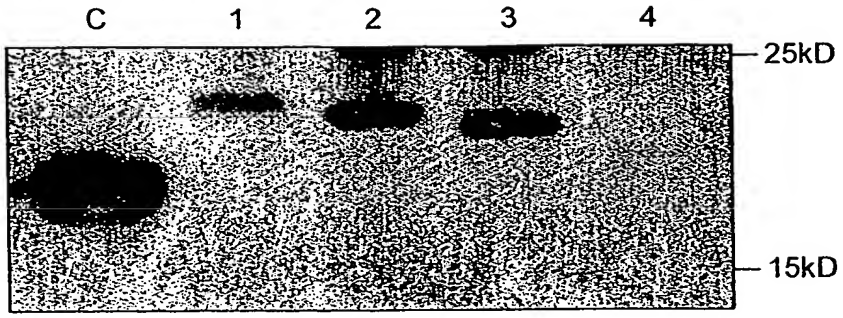
C
1
2
3
4
25kD
15kD

FIG. 16

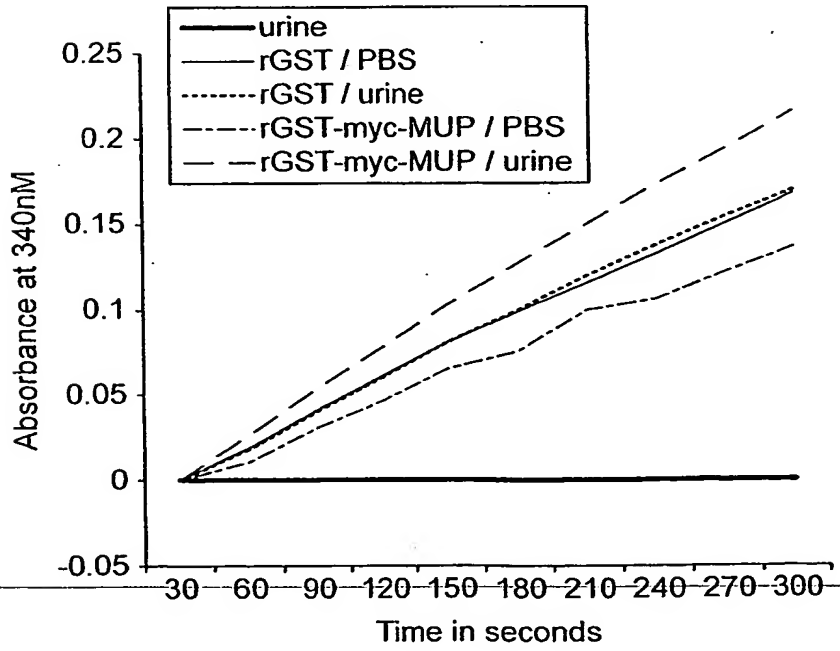
urine
rGST / PBS
rGST / urine
rGST-myc-MUP / PBS
rGST-myc-MUP / urine
0.25
0.2
0.15
0.1
0.05
0
-0.05
Absorbance at 340nM
30
60
90
120
150
180
210
240
270
300
Time in seconds

FIG. 17

FIG. 18

```
1     gtgctcagca acacacccag caccagcatt cccgctgctc ctgaggtctg caggcagctc
61    gctgtagcct gagcggtgtg gagggaagtg tcctgggaga tttaaaatgt gagaggcggg
121   aggtgggagg ttgggccctg tgggcctgcc catcccacgt gcctgcatta gccccagtgc
181   tgctcagccg tgcccccgcc gcaggggtca ggtcactttc ccgtcctggg gttattatga
241   ctcttgtcat tgccattgcc atttttgcta ccctaactgg gcagcaggtg cttgcagagc
301   cctcgatacc gaccaggtcc tccctcggag ctcgacctga accccatgtc acccttgccc
361   cagcctgcag agggtgggtg actgcagaga tcccttcacc caaggccacg gtcacatggt
421   ttggaggagc tggtgcccaa ggcagaggcc accctccagg acacacctgt ccccagtgct
481   ggctctgacc tgtccttgtc taagaggctg accccggaag tgttcctggc actggcagcc
541   agcctggacc cagagtccag acacccacct gtgcccccgc ttctggggtc taccaggaac
601   cgtctaggcc cagaggggga cttcctgctt ggccttggat ggaagaaggc ctcctattgt
661   cctcgtagag gaagccaccc cggggcctga ggatgagcca agtgggattc cgggaaccgc
721   gtggctgggg gcccagcccg ggctggctgg cctgcatgcg cctcctgtat aaggccccaa
781   gcctgcctgt ctcagccctc cactccctgc agagctcaga agcacgaccc cagctgcagc
841   catgaagtgc ctcctgcttg ccctgggcct ggccctcgcc tgtggcgtcc aggccatcat
901   cgtcacccag accatgaaag gcctggacat ccagaaggtt cgagggttgg ccgggtgggt
961   gagttgcagg gcgggcaggg gagctgggcc tcagagagcc aagagaggct gtgacgttgg
1021  gttcccatca gtcagctagg gccacctgac aaatccccgc tggggcagct tcaaccaggc
1081  gttcactgtc ttgcattctg gaggctggaa gccccaagatc caggtgttgg cagggctggc
1141  ttctcctgcg gccgctctct ggggagcaga cggccgtctt ctccagtcct ctgcgcgccc
1201  tgatttcctc ttcctgtgag gccaccaggc ctgctggaaa cacgcctgcc tgcgcagctt
1261  cacacgacct ttgtcatctc tttaaaggcc atgtctccag agtcatgtgt tgaagttctg
1321  ggggttagtg ggacacagtt cagcccctaa aagagtctct ctgcccctca aattttcccc
1381  acctccagcc atgtctcccc aagatccaaa tgttgctaca tgtgggggg ctcatctggg
1441  tccctctttg ggttcagtgt gagtctgggg agagcattcc ccagggtgca gagttggggg
1501  gagtatctca gggctgccca ggccggggtg ggacagagag cccactgtgg ggctgggggc
1561  cccttcccac ccccagagtg caactcaagg tccctctcca ggtggcgggg acttggcact
1621  ccttggctat ggcggccagc gacatctccc tgctggatgc ccagagtgcc cccctgagag
1681  tgtacgtgga ggagctgaag cccacccccg agggcaacct ggagatcctg ctgcagaaat
1741  ggtgggcgtc tctccccaac atggaacccc cactccccag ggctgtggac cccccggggg
1801  gtggggtgca ggagggacca gggccccagg gctggggaag agggctcaga gtttactggt
1861  acccggcgct ccacccaagg ctgcccaccc agggcttttt ttttttttaa acttttatta
1921  atttgatgct tcagaacatc atcaaacaaa tgaacataaa acattcattt ttgtttactt
1981  ggaaggggag ataaaatcct ctgaagtgga aatgcatagc aaagatacat acaatgaggc
2041  aggtattctg aattccctgt tagtctgagg attacaagtg tatttgagca acagagagac
2101  attttcatca tttctagtct gaacacctca gtatctaaaa tgaacaagaa gtcctggaaa
2161  cgaagcagtg tggggatagg cccgtgtgaa ggctgctggg aggcagcaga cctgggtctt
2221  cgggctcaag cagttcccgc taccagccct gtccacctca gacgggggtc agggtgcagg
2281  agagagctgg atgggtgtgg gggcagagat ggggacctga accccagggc tgccttttgg
2341  gggtgcctgt ggtcaaggct ctccctgacc ttttctctct ggcttcatct gacttctcct
2401  ggcccatcca cccggtcccc tgtggcctga ggtgacagtg agtgcgccga ggctagttgg
2461  ccagctggct cctatgccca tgccaccccc ctccagccct cctgggccag cttctgcccc
2521  tggccctcag ttcatcctga tgaaaatggt ccatgccaat ggctcagaaa gcagctgtct
2581  ttcagggaga acggcgagtg tgctcagaag aagattattg cagaaaaaac caagatccct
2641  gcggtgttca agatcgatgg tgagtccggg tccctggggg acacccacca cccccgcccc
2701  cggggactgt ggacaggttc agggggctgg cgtcgggccc tgggatgcta agggactggt
2761  ggtgatgaag acactgcctt gacacctgct tcacttgcct cccctgccac ctgcccgggg
2821  ccttggggcg gtggccatgg gcaggtcccg gctggcgggc taacccacca gggtgacacc
2881  cgagctctct ttgctggggg gcgggcggtg ctctgggccc tcaggctgag ctcaggaggt
2941  acctgtgccc tcccaggggt aaccgagagc cgttgcccac tccaggggcc caggtgcccc
3001  acgaccccag cccgctccac agctccttca tctcctggag acaaactctg tccgccctcg
3061  ctcattcact tgttcgtcct aaatccgaga tgataaagct tcgaggggg gttggggttc
3121  catcagggct gcccttccgc cgggcagcct gggccacatc tgcccttggc cccctcagga
3181  ctcactctga ctggaggccc tgcactgact gacgccaggg tgcccagccc agggtctctg
3241  gcgccatcca gctgcactgg gtttgggtgc tggtcctgcc cccaagctgc ccggacacca
3301  caggcagccg gggctgccca ctggcctcgg tcagggtgag ccccagctgc ccccgctcag
3361  ggcttgcccc gacaatgacc ccatcctcag gacgcacccc ccttcccttg ctgggcagtg
3421  tccagcccca cccgagatcg ggggaagccc tatttcttga caactccagt ccctgggga
3481  gggggcctca gactgagtgg tgagtgttcc caagtccagg aggtggtgga gggtcctggc
3541  ggatccagag ttgacagtga gggcttcctg ggccccatgc gcctggcagt ggcagcaggg
3601  aagaggaagc accatttcag gggtggggga tgccagaggc gctccccacc ccgtcttcgc
```

```
3661  cgggtggtga ccccggggga gccccgctgg tcgtggaggg tgctgggggc tgactagcaa
3721  cccctccccc cccgttggaa ctcacttttc tcccgtcttg accgcgtcca gccttgaatg
3781  agaacaaagt ccttgtgctg gacaccgact acaaaaagta cctgctcttc tgcatggaaa
3841  acagtgctga gcccgagcaa agcctggcct gccagtgcct gggtgggtgc caaccctggc
3901  tgcccaggga gaccagctgc gtggtccttg ctgcaacagg gggtgggggg tgggagcttg
3961  atccccagga ggaggagggg tggggggtcc ctgagtcccg ccaggagaga gtggtcgcat
4021  accgggagcc agtctgctgt gggcctgtgg gtggctgggg acgggggcca gacacacagg
4081  ccgggagacg ggtgggctgc agaactgtga ctggtgtgac cgtcgcgatg gggccggtgg
4141  tcactgaatc taacagcctt tgttaccggg gagtttcaat tatttcccaa aataagaact
4201  caggtacaaa gccatctttc aactatcaca tcctgaaaac aaatggcagg tgacattttc
4261  tgtgccgtag cagtcccact gggcattttc agggcccctg tgccaggggg gcgcgggcat
4321  cggcgagtgg aggctcctgg ctgtgtcagc cggcccaggg ggaggaaggg acccggacag
4381  ccagaggtgg ggggcaggct ttccccctgt gacctgcaga cccactgcac tgccctggga
4441  ggaagggagg ggaactaggc caaggggaa gggcaggtgc tctggagggc aagggcagac
4501  ctgcagacca ccctggggag cagggactga cccccgtccc tgccccatag tcaggacccc
4561  ggaggtggac aacgaggccc tggagaaatt cgacaaagcc ctcaaggccc tgcccatgca
4621  catccggctt gccttcaacc cgacccagct ggagggtgag cacccaggcc ccgcccttcc
4681  ccagggcagg agccacccgg ccccgggacg acctcctccc atggtgaccc ccagctcccc
4741  aggcctccca ggaggaaggg gtggggtgca gcaccccgtg ggggccccct ccccaccccc
4801  tgccaggcct ctcttcccga ggtgtccagt cccatcctga ccccccccatg actctccctc
4861  ccccacaggg cagtgccacg tctaggtgag cccctgccgg tgcctctggg gtaagctgcc
4921  tgccctgccc cacgtcctgg gcacacacat ggggtagggg gtcttggtgg ggcctgggac
4981  cccacatcag gccctggggt ccccccctgtg agaatggctg gaagctgggg tccctcctgg
5041  cgactgcaga gctggctggc cgcgtgccac tcttgtgggt gacctgtgtc ctggcctcac
5101  acactgacct cctccagctc cttccagcag agctaaggct aagtgagcca gaatggtacc
5161  taaggggagg ctagcggtcc ttctcccgag gaggggctgt cctggaacca ccagccatgg
5221  agaggctggc aagggtctgg caggtgcccc aggaatcaca ggggggcccc atgtccattt
5281  cagggcccgg gagccttgga ctcctctggg gacagacgac gtcaccaccg ccccccccc
5341  atcaggggga ctagaaggga ccaggactgc agtcaccctt cctgggaccc aggcccctcc
5401  aggcccctcc tggggctcct gctctgggca gcttctcctt caccaataaa ggcataaacc
5461  tgtgctctcc cttctgagtc tttgctggac gacgggcagg gggtggagaa gtggtgggga
5521  gggagtctgg ctcagaggat gacagcgggg ctgggatcca gggcgtctgc atcacagtct
5581  tgtgacaact gggggcccac acacatcact gcggctcttt gaaactttca ggaaccaggg
5641  agggactcgg cagagacatc tgccagttca cttggagtgt tcagtcaaca cccaaactcg
5701  acaaaggaca gaaagtggaa aatggctgtc tcttagtcta ataaatattg atatgaaact
5761  caagttgctc atggatcaat atgcctttat gatccagcca gccactactg tcgtatcaac
5821  tgatgtaccc aaacgcactg atctgtctgg ctaatgatga gagattccca gtagagagct
5881  ggcaagaggt cacagtgaga actgtctgca cacacagcag agtccaccag tcatcctaag
5941  gagatcagtc ctggtgttca ttggaggact gatgttgaag ctgaaactcc aatgctttgg
6001  ccacctgatg tgaagagctg actcatttga aaagaccctg atgctgggaa agattgaggg
6061  caggaggaga aggggacgac agaggatgag atggttggat ggcatcacca acacaatgga
6121  catgggtttg ggtggactcc aggagttggt gatggacagg gaggcctggc gtgctacgga
6181  agcggtttat ggggtcacaa agactgagtg actgaactga gctgaactga atggaaatga
6241  ggtatacagc aaagtgggga ttttttagat aataagaata tacacataac atagtgtata
6301  ctcatatttt tatgcatacc tgaatgctca gtcactcagt cgtatctgac tctgtgacct
6361  atggaccgta gccttccagg tttcttctgt ccacagaatt ctccaaggca agaatactgg
6421  agtgggtagc catttcctcc tccaggggat cctcccgacc cagggattga accggcatct
6481  cctgtattgg caggtggatt ctttaccact gtgccaccag ggaagcccgt gttactctct
6541  atgtcccact taattaccaa agctgctcca agaaaaagcc cctgtgccct ctgagcttcc
6601  cggcctgcag agggtggtgg gggtagactg tgacctggga acaccctccc gcttcaggac
6661  tcccgggcca cgtgacccac agtcctgcag acagccgggt agctctgctc ttcaaggctc
6721  attatcttta aaaaaaactg aggtctattt tgtgacttcg ctgccgtaac ttctgaacat
6781  ccagtgcgat ggacaggacc tcctccccag gcctcagggg cttcagggag ccagccttca
6841  cctatgagtc accagacact cgggggtggc cccgccttca gggtgctcac agtcttccca
6901  tcgtcctgat caaagagcaa gaccaatgac ttcttaggag caagcagaca cccacaggac
6961  actgaggttc accagagctg agctgtcctt ttgaacctaa agacacacag ctctcgaagg
7021  ttttctcttt aatctggatt taaggcctac ttgcccctca agagggaaga cagtcctgca
7081  tgtccccagg acagccactc ggtggcatcc gaggccactt agtattatct gaccgcaccc
7141  tggaattaat cggtccaaac tggacaaaaa ccttggtggg aagtttcatc ccagaggcct
7201  caaccatcct gctttgacca ccctgcatct ttttttcttt tatgtgtatg catgtatata
7261  tatatatata ttttttttttt tttcattttt tggctgtgct ggctgttcgt tgcagttcgg
7321  tgcgcaggct tctctctagt ttctctctag tcttctctta tcacagagca gtctctaga
```

FIG. 18 CONT'D

MKCLLLALGLALACGVQAIIVTQTMKGLDIQKVAGTWHSLAMAA
SDISLLDAQSAPLRVYVEELKPTPEGNLEILLQKWENGECAQKKIIAEKTKIPAVFKI
DALNENKVLVLDTDYKKYLLFCMENSAEPEQSLACQCLVRTPEVDNEALEKFDKALKA
LPMHIRLAFNPTQLEGQCHV

FIG. 19

```
1     ctgaacccag agagtatata agaacaagca aaggggctgg ggagtggagt gtagccacga
61    tcacaagaaa gacgtggtcc tgacagacag acaatcctat tccctaccaa aatgaagatg
121   ctgctgctgc tgtgtttggg actgacccta gtctgtgtcc atgcagaaga agctagttct
181   acgggaagga actttaatgt agaaaagatt aatggggaat ggcatactat tatcctggcc
241   tctgacaaaa gagaaaagat agaagataat ggcaacttta gacttttttct ggagcaaatc
301   catgtcttgg agaattcctt agttcttaaa ttccatactg taagagatga agagtgctcg
361   gaattatcta tggttgctga caaaacagaa aaggctggtg aatattctgt gacgtatgat
421   ggattcaata catttactat acctaagaca gactatgata actttcttat ggctcatctc
481   attaacgaaa aggatgggga aaccttccag ctgatggggc tctatggccg agaaccagat
541   ttgagttcag acatcaagga aaggtttgca caactatgtg agaagcatgg aatccttaga
601   gaaaatatca ttgacctatc caatgccaat cgctgcctcc aggcccgaga atgaagaatg
661   gcctgagcct ccagtgttga gtggagactt ctcaccagga ctccaccatc atcccttcct
721   atccatacag catccccagt ataaattctg tgatctgcat tccatcctgt ctcactgaga
781   agtccaattc cagtctatcc acatgttacc taggatacct catcaagaat caaagacttc
841   tttaaatttt tctttgatat acccatgaca atttttcatg aatttcttcc tcttcctgtt
901   caataaatga ttacccttgc actta
```

FIG. 20

MKMLLLLCLGLTLVCVHAEEASSTGRNFNVEKINGEWHTIILAS
DKREKIEDNGNFRLFLEQIHVLENSLVLKFHTVRDEECSELSMVADKTEKAGEYSVTY
DGFNTFTIPKTDYDNFLMAHLINEKDGETFQLMGLYGREPDLSSDIKERFAQLCEKHG
ILRENIIDLSNANRCLQARE

FIG. 21

```
1     ctgctgctgc tgtgtctgcg cctgacactg gtctgtggcc atgcagaaga agctagttcc
61    acaagaggga acctcgatgt ggctaagctc aatggggatt ggttttctat tgtcgtggcc
121   tctaacaaaa gagaaaagat agaagagaat ggcagcatga gagtttttat gcagcacatc
181   gatgtcttgg agaattcctt aggcttcaag ttccgtatta aggaaaatgg agagtgcagg
241   gaactatact tggtttccta caaaacgcca gaggatggtg aatattttgt tgagtatgac
301   ggagggaata catttactat acttaagaca gactactaca tatacgtcat gtttcatctc
361   attaatttca agaacgggga aaccttccag ctgatggtgc tctacggcag aacaaaggat
421   ctgagttcag acatcaagga aaagtttgca aaactatgtg aggcgcatgg aatcactagg
481   gacaatatca ttgatctaac caagactgat cgctgtctcc aggcccgagg atgaagaaag
541   gcctgagcct ccagtgctga gtggagactt ctcaccagga ctctagcatc accatttcct
601   gtccatggag catcctgaga caaattctgc gatctgattt ccatcctctg tcacagaaaa
661   gtgcaatcct ggtctctcca gcatcttccc tagttaccca ggacaacaca tcgagaatta
721   aaagctttct taaatttctc ttggccccac ccatgatcat tccgcacaaa tatcttgctc
781   ttgcagttca ataaatgatt acccttgcac ttt
```

FIG. 22

atgtcccctatactaggttattggaaaattaagggccttgtgcAacccactcgacttcttttggaatatcttgaagaaaaatatga
agagcatttgtatgagcgcgatgaaggtgataaatggcgaaacAaaaagtttgaattgggtttggagtttcccaatcttcctta
ttatattgatggtgatgttaaattaacacagtctatggccatcatacgttatatagctgacaagcacaacatgttgggtggttgtc
caaaagagcgtgcagagatttcaatgcttgaaggagcggttttggatattagatacggtgtttcgagaattgcatatagtaaa
gactttgaaactctcaaagttgattttcttagcaagctacctgaaatgctgaaaatgttcgaagatcgtttatgtcataaaacatat
ttaaatggtgatcatgtaacccatcctgacttcatgttgtatgacgctcttgatgttgttttatacatggacccaatgtgcctggat
gcgttcccaaaattagtttgttttaaaaaacgtattgaagctatcccacaaattgataagtacttgaaatccagcaagtatatagc
atggcctttgcagggctggcaagccacgtttggtggtggcgaccatcctccaaaatcggatctggaagttctgttccagggg
cccctgggatccccggaattcccgggtcgactcgagcggccgcatcgtgactga

		Met Ser Pro Ile Leu Gly Tyr Trp
241		ATG TCC CCT ATA CTA GGT TAT TGG
	Lys Ile Lys Gly Leu Val Gln Pro Thr Arg Leu Leu Leu	
281	AAA ATT AAG GGC CTT GTG CAA CCC ACT CGA CTT CTT TTG	
	Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu Tyr Glu Arg	
321	GAA TAT CTT GAA GAA AAA TAT GAA GAG CAT TTG TAT GAG CGC	
	Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
361	GAT GAA GGT GAT AAA TGG CGA AAC AAA AAG TTT GAA TTG	
	Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly	
401	GGT TTG GAG TTT CCC AAT CTT CCT TAT TAT ATT GAT GGT	
	Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile	
441	GAT GTT AAA TTA ACA CAG TCT ATG GCC ATC ATA CGT TAT ATA	
	Ala Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu	
481	GCT GAC AAG CAC AAC ATG TTG GGT GGT TGT CCA AAA GAG	
	Arg Ala Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp	
521	CGT GCA GAG ATT TCA ATG CTT GAA GGA GCG GTT TTG GAT	
	Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe	
561	ATT AGA TAC GGT GTT TCG AGA ATT GCA TAT AGT AAA GAC TTT	
	Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
601	GAA ACT CTC AAA GTT GAT TTT CTT AGC AAG CTA CCT GAA	
	Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr	
641	ATG CTG AAA ATG TTC GAA GAT CGT TTA TGT CAT AAA ACA	
	Tyr Leu Asn Gly Asp His Val Thr His Pro Asp Phe Met Leu	
681	TAT TTA AAT GGT GAT CAT GTA ACC CAT CCT GAC TTC ATG TTG	
	Tyr Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met	
721	TAT GAC GCT CTT GAT GTT GTT TTA TAC ATG GAC CCA ATG	
	Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys Lys	
761	TGC CTG GAT GCG TTC CCA AAA TTA GTT TGT TTT AAA AAA	
	Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser	
801	CGT ATT GAA GCT ATC CCA CAA ATT GAT AAG TAC TTG AAA TCC	
	Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
841	AGC AAG TAT ATA GCA TGG CCT TTG CAG GGC TGG CAA GCC	
	Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu	
881	ACG TTT GGT GGT GGC GAC CAT CCT CCA AAA TCG GAT CTG	
	Glu Val Leu Phe Gln Gly Pro Leu	
921	GAA GTT CTG TTC CAG GGG CCC CTG	

FIG. 23